

Fig. 1A

Gene Target (A658):	CMV/CBA	GFP*	IRES	CD8	WPRE	PGK-NEO
<i>Stop-Sce site</i>						
Repair Substrate (RS2100):	37	truncGFP	IRES	CD8		
Repair Substrate (RS2700):	37	truncGFP	IRES	CD8	WPRE	

Fig. 1B

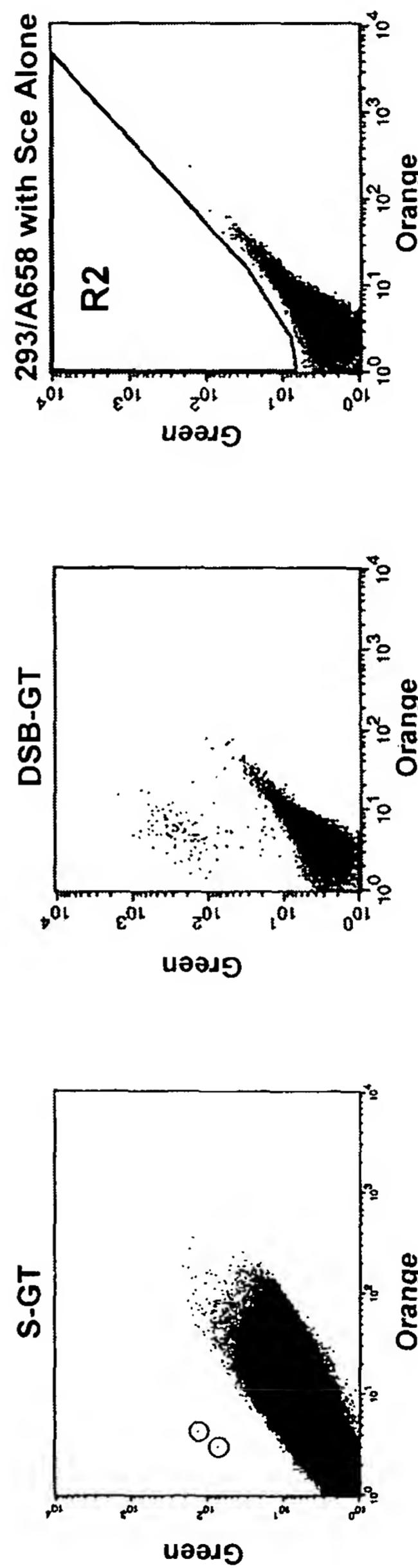


Fig. 1C

Gene Target		1 bp insertion		7 bp insertion		35 bp insertion		66 bp insertion (A658)		66 bp insertion (QQR8)		Fold Stimulation By Sce Induced DSB	
Sce	No	No	No	No	No	No	No	Yes	Yes	Yes	Yes	Yes	Yes
Events/ 10 <sup>6</sup> cells	29.5 +/- 13.0		1.5 +/- 1.1		0.71 +/- 0.27		1600 +/- 500		1900 +/- 250		>2000		
Rate	2.9 x 10 <sup>-5</sup>		1.5 x 10 <sup>-6</sup>		7.1 x 10 <sup>-7</sup>		1.6 x 10 <sup>-3</sup>		1.9 x 10 <sup>-3</sup>				

Fig. 1D

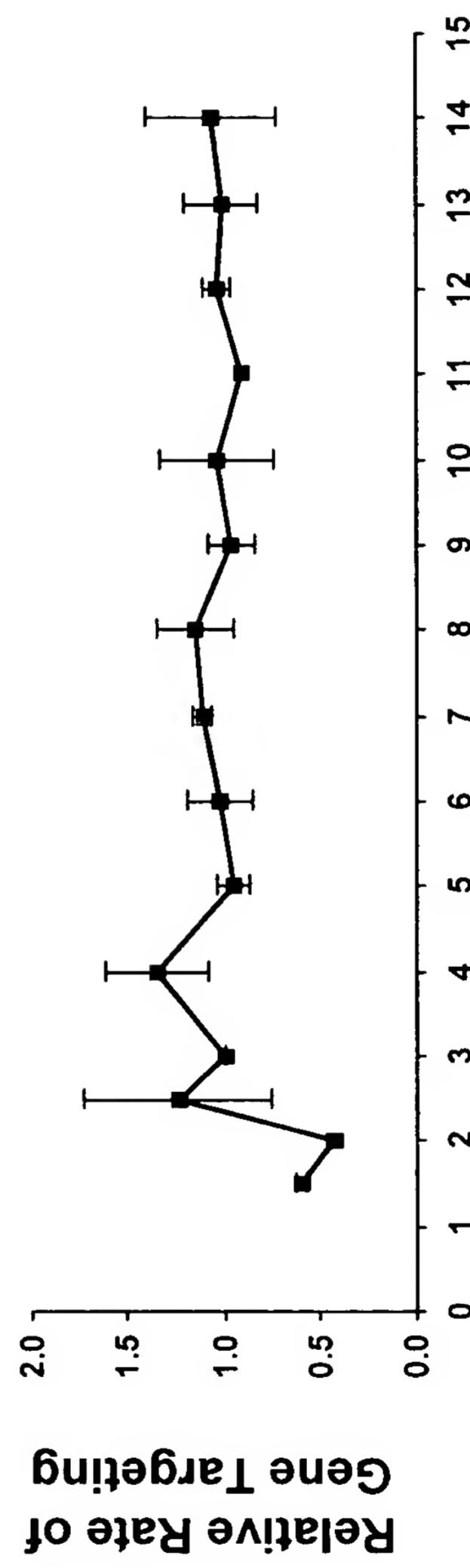


Fig. 2A

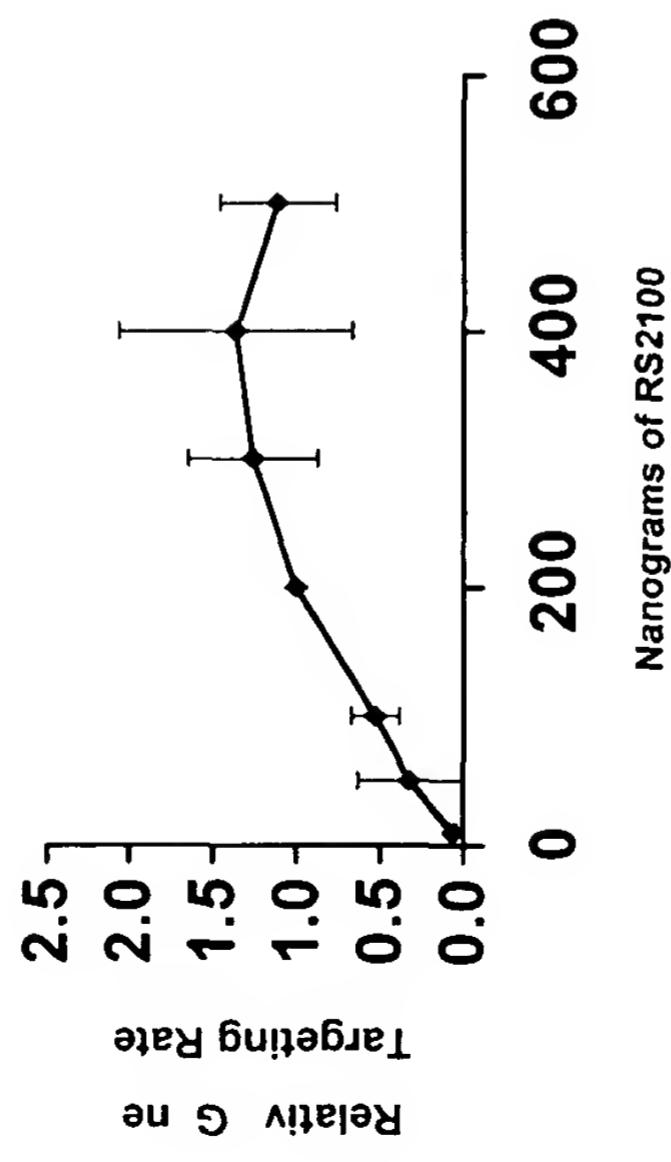


Fig. 2B

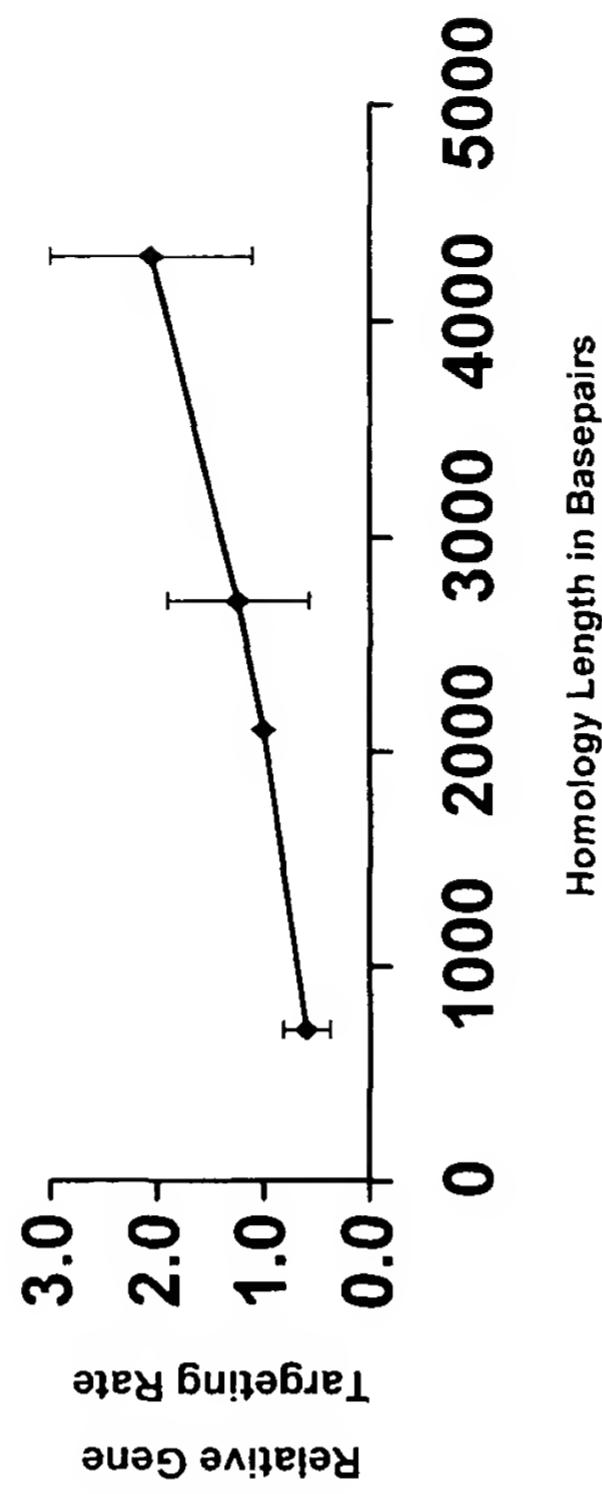


Fig. 2C

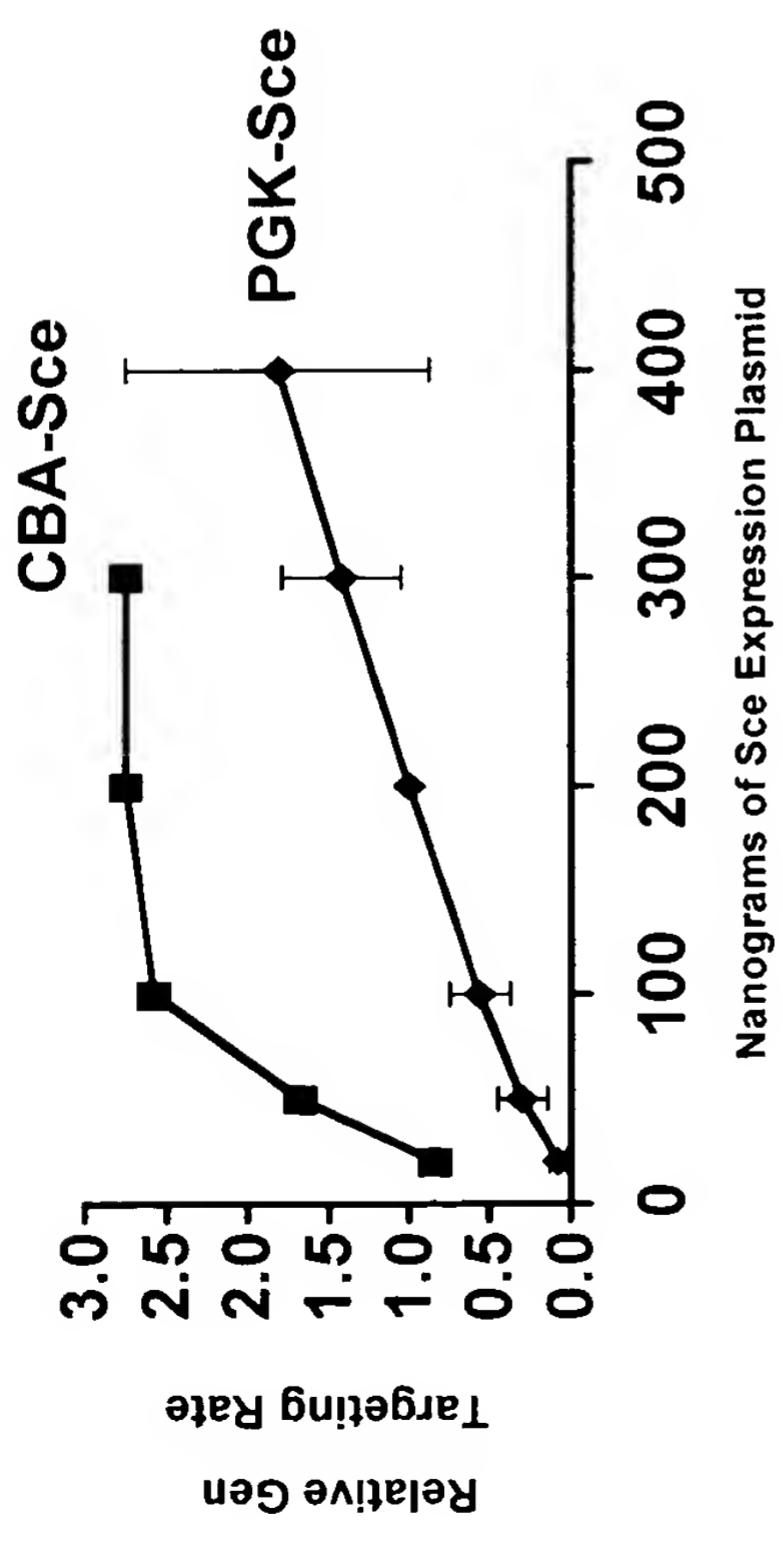


Fig. 2D

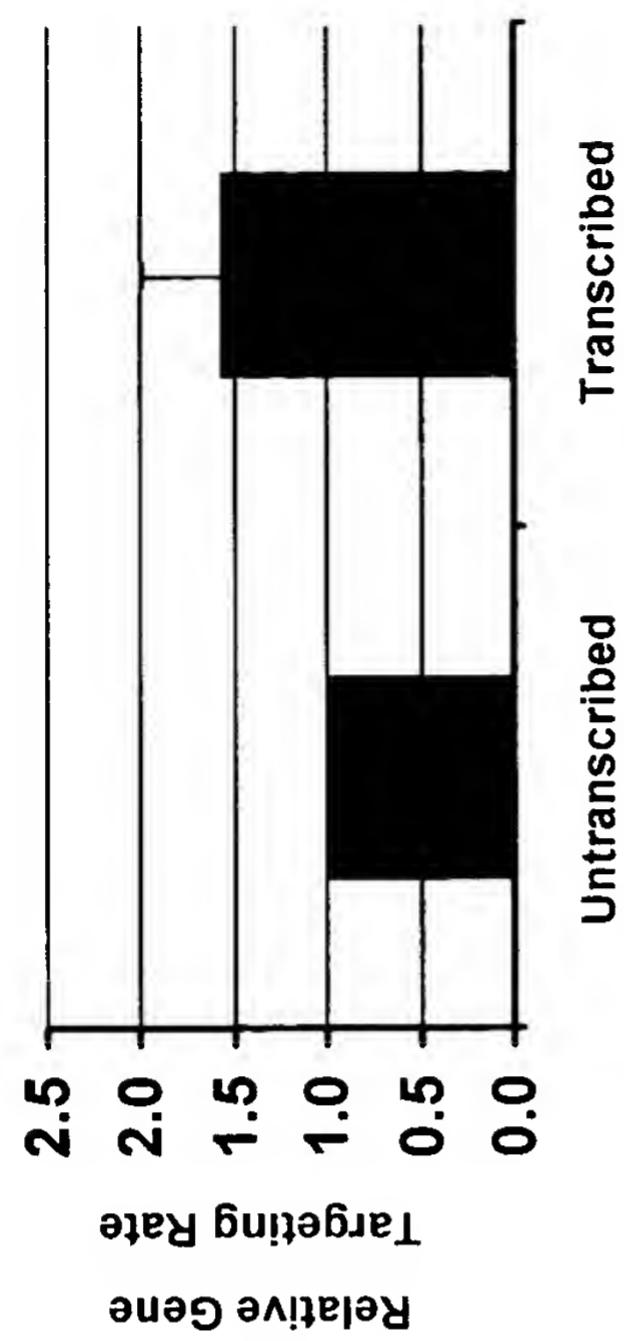


Fig. 2E

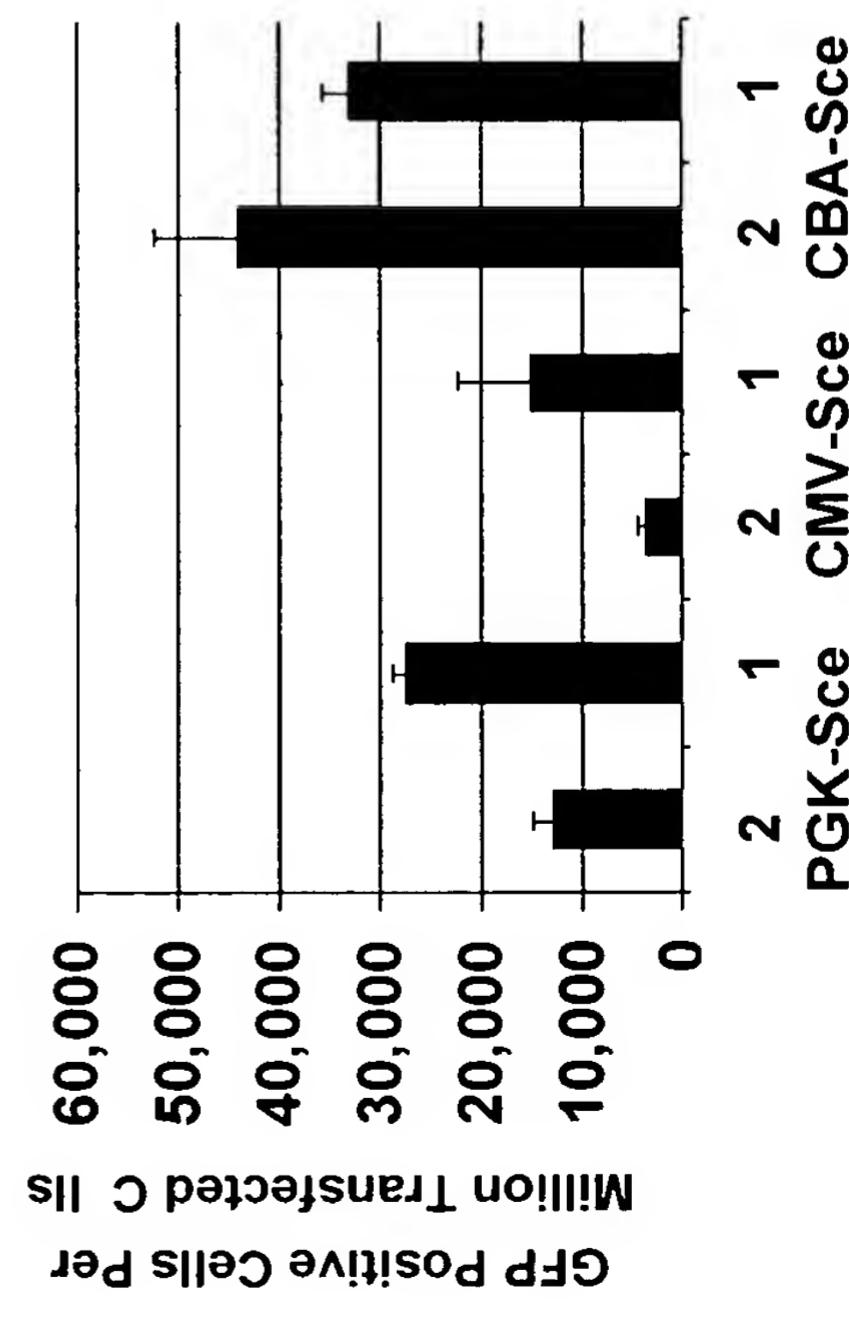


Fig. 3A

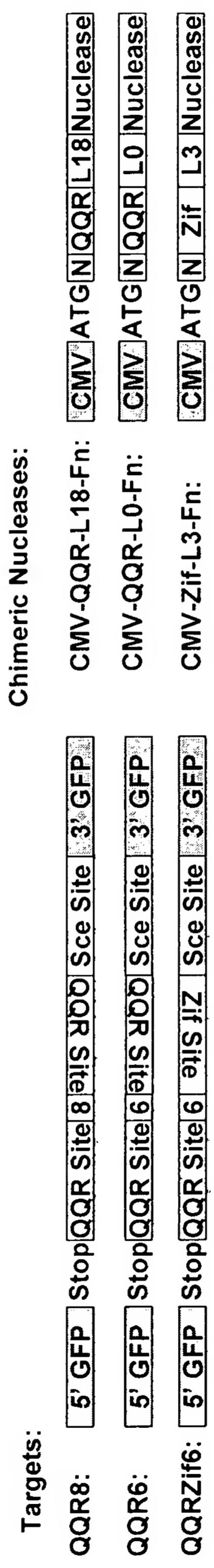


Fig. 3B

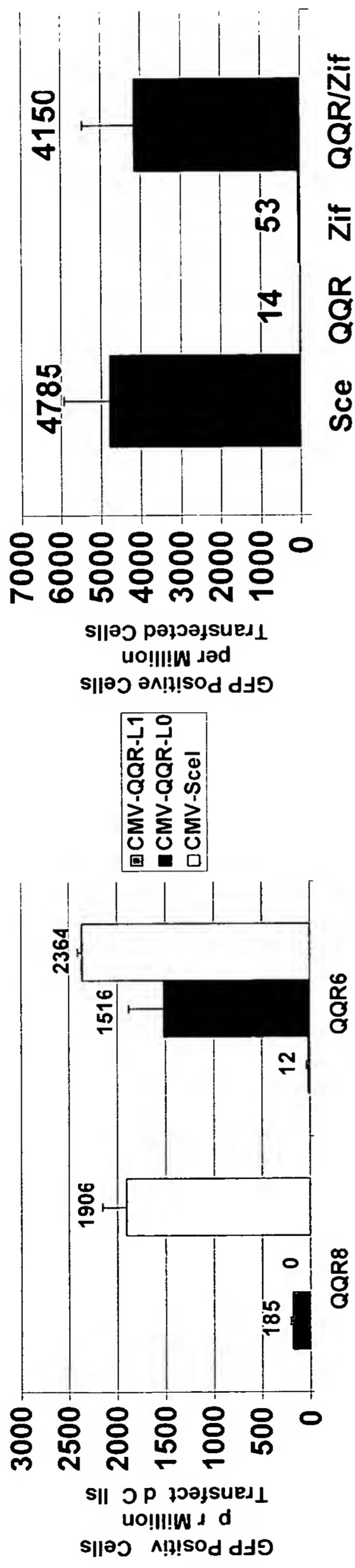


Fig. 3C

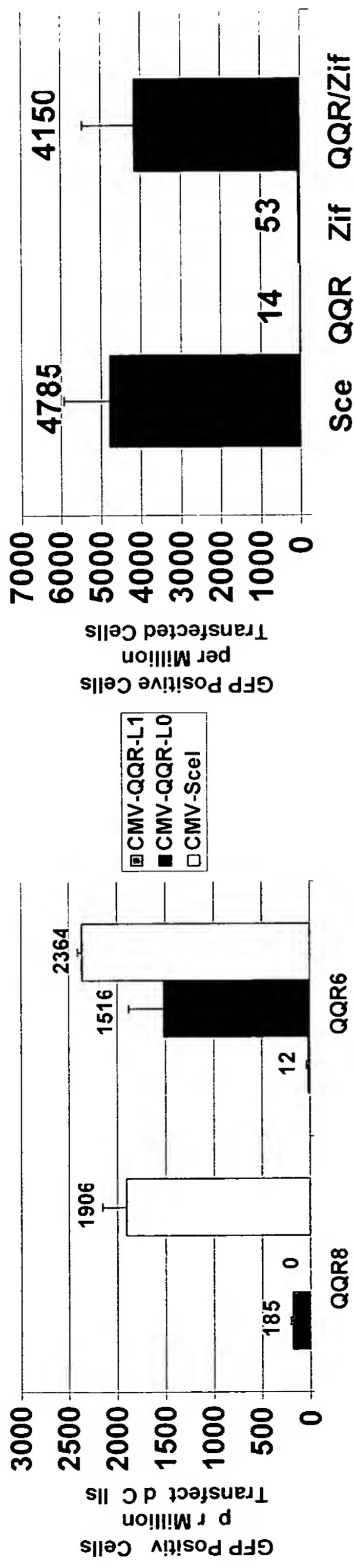


Fig. 3D

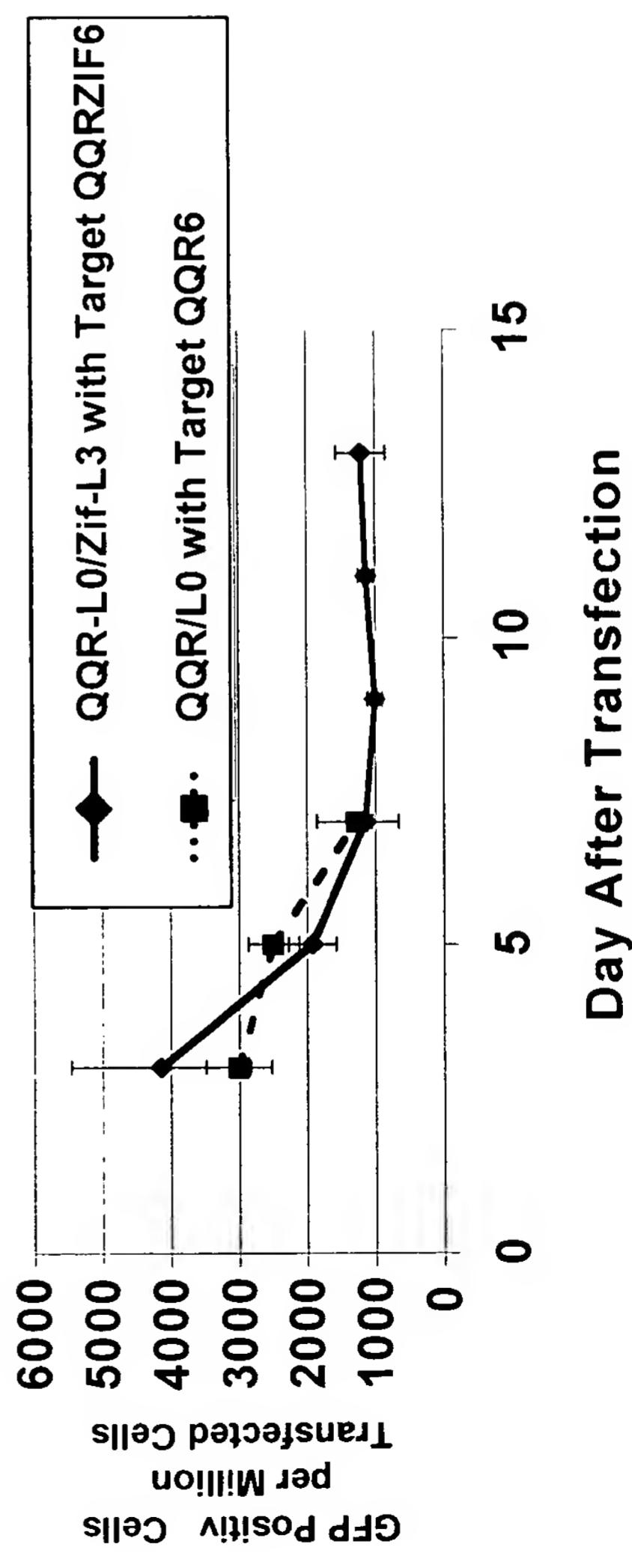


Fig. 4

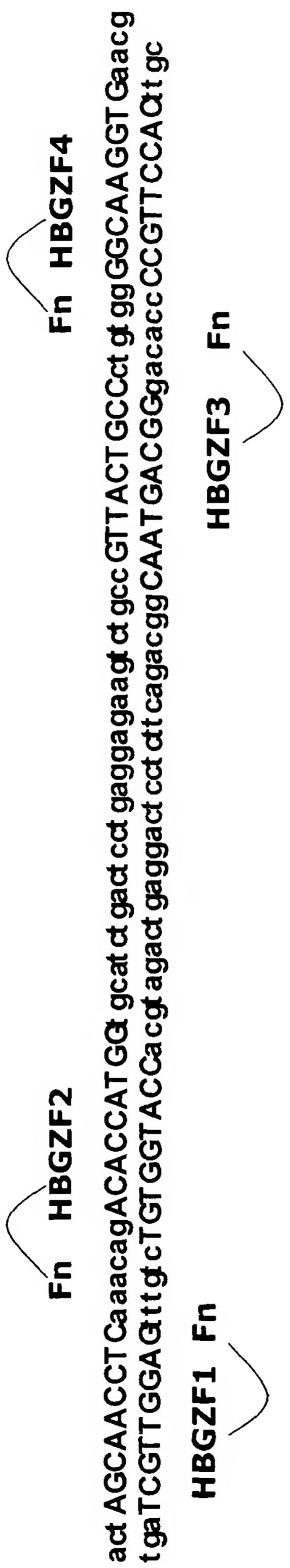


Fig. 5

## Design of HBGZF1

**Target Binding Site:** 5' GAG GTT GCT 3'

F3 F2 F1

-1 1 2 3 4 5 6  
B3 B2 B1

Finger 1: GCT Q S S D L T R  
T S G E L V R

Finger 2 GTT T S G A L T R  
T S G S L T R

Finger 3: GAG R S D N L T R  
R S D N L V R

**Structure of CMV-HBGZF1**



ATG-NLS-FLAG-Finger 1(QSSSDLTR)-Finger2(TSGALTR)-Finger3(RSDNLTR)-Fn

Fig. 6

## Gene Targeting with HBGZF1

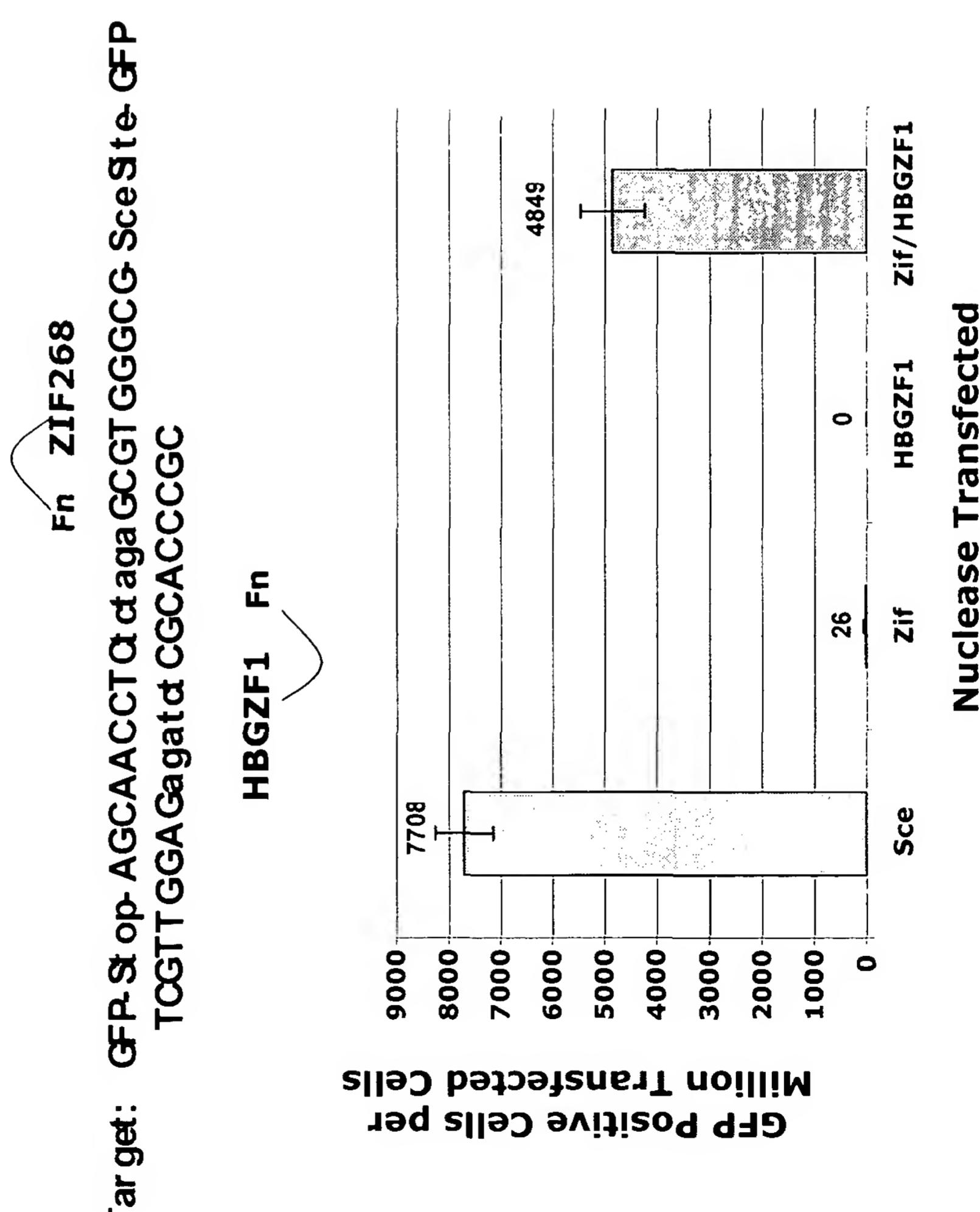


Fig. 7

## Design of HBGZF4

Target Binding Site: 5' GGC AAG GTG 3'

F3 F2 F1

-1 1 2 3 4 5 6  
B3 B2 B1

Finger 1: GTG R S D A L T R  
R S N S L T R

Finger 2 AAG R S D T L S N  
R K D N L K N  
R S S N L T Q

Finger 3 GGC D R S H L A R  
E S N H L T R  
E R S K L A R  
D P G H L V R

### Structure of CMV-HBGZF1



ATG-NLS-FLAG-Finger 1(RSDALTR)-Finger2(RSSNLTQ)-Finger3(DRSHLAR)-Fn

Fig. 8

## Gene Targeting with HBGZF4

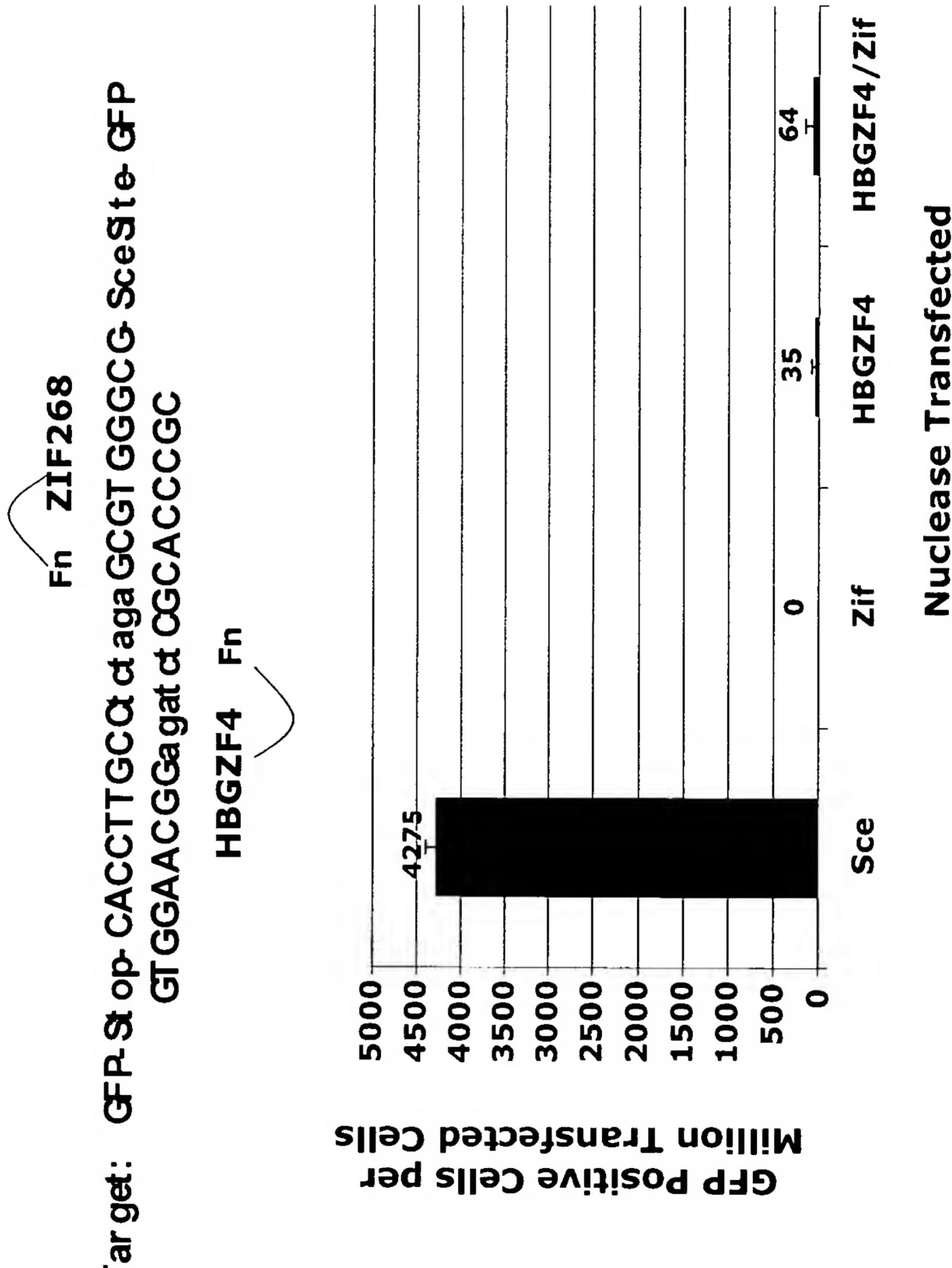


Fig. 9A

## Human Common Gamma Chain Deficiency

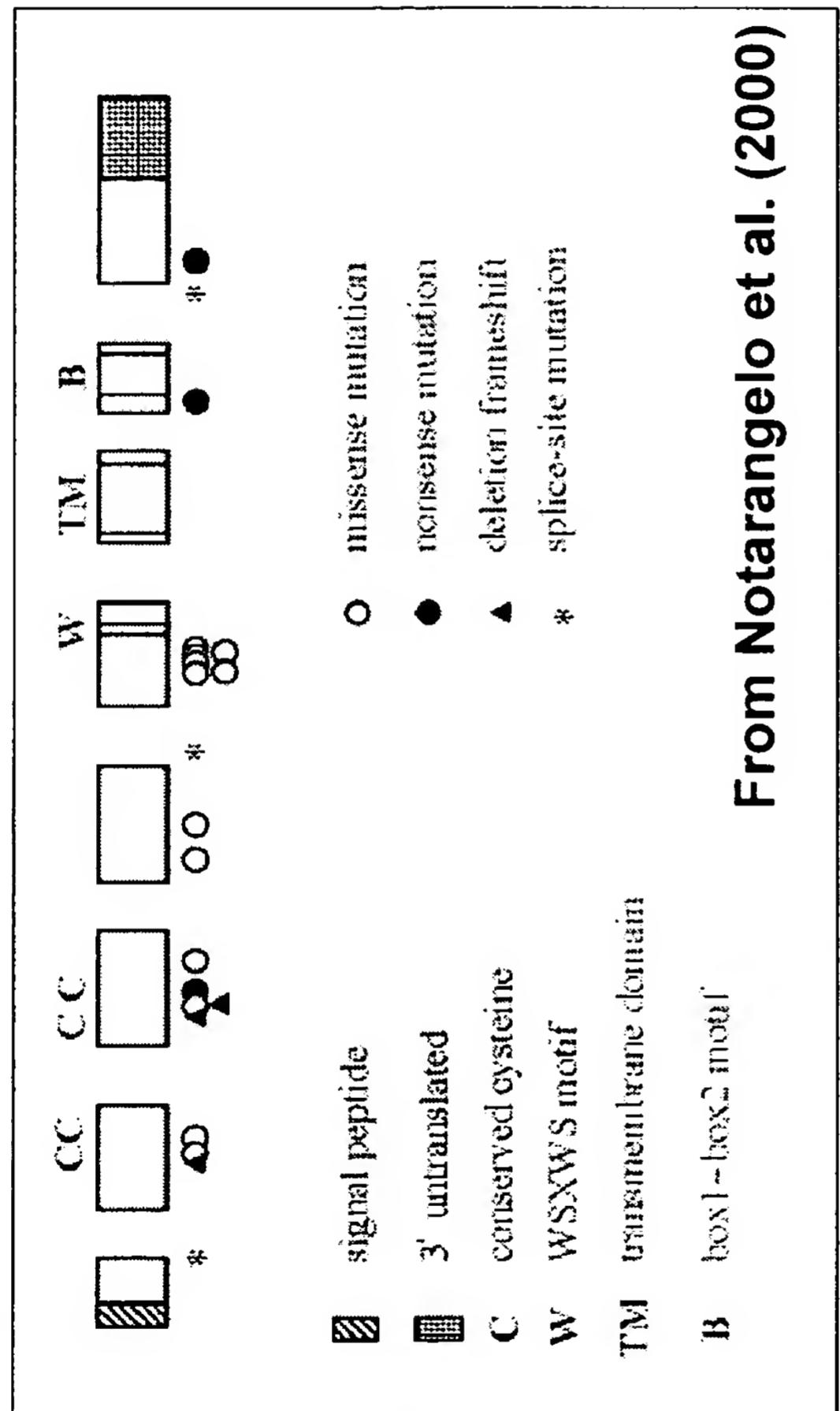


Fig. 9B

## Exon 5

5' gaacaat cagt ggatt at agacat aagt ct cttt gcct agt gt ggtt gggcagaaac gct acacgtt cgt gt  
3' ct t gtt agt cacct aat at ct g at caaggaaacggat cacacct acccg ttt gcgtt gtt gcaaaagccaa  
HCGCZF2  
WSXWS motif  
cgaggccgctt aaccact ct gt ggaagt gct cagcatt ggat tt aaccct ccact gggggagcca  
gcct cggcggaaatt gggt gagacacctt cacgagt ct aacct cact tacct cggt gggtt aggt gacccct cgt  
HCGCZF1  
at actt caaaaagag 3'  
tat gaagttt ct g 5'

Fig. 10

## Design of HCGCZF2

Target Binding Site: 5' GGG GGA GCA 3'  
F3 F2 F1

-1 1 2 3 4 5 6  
B3 B2 B1

Finger 1: GCA Q S G S L T R  
Q S G D L T R  
Q S G D L T R  
Q S N D L T R\*

Finger 2 GGA Q S G H L Q K  
Q R A H L E R  
Q S S H L T R\*

Finger 3: GGG R S D H L A R  
R S D H L T R  
R S S H L T R\*

### Structure of CMV-HCGCZF2



ATG-NLS-FLAG-Finger 1(QSNDLTR)-Finger2(QSSHDLTR)-Finger3(RSSHDLTR)-Fn

Fig. 11

## Gene Targeting with HCGCZF2

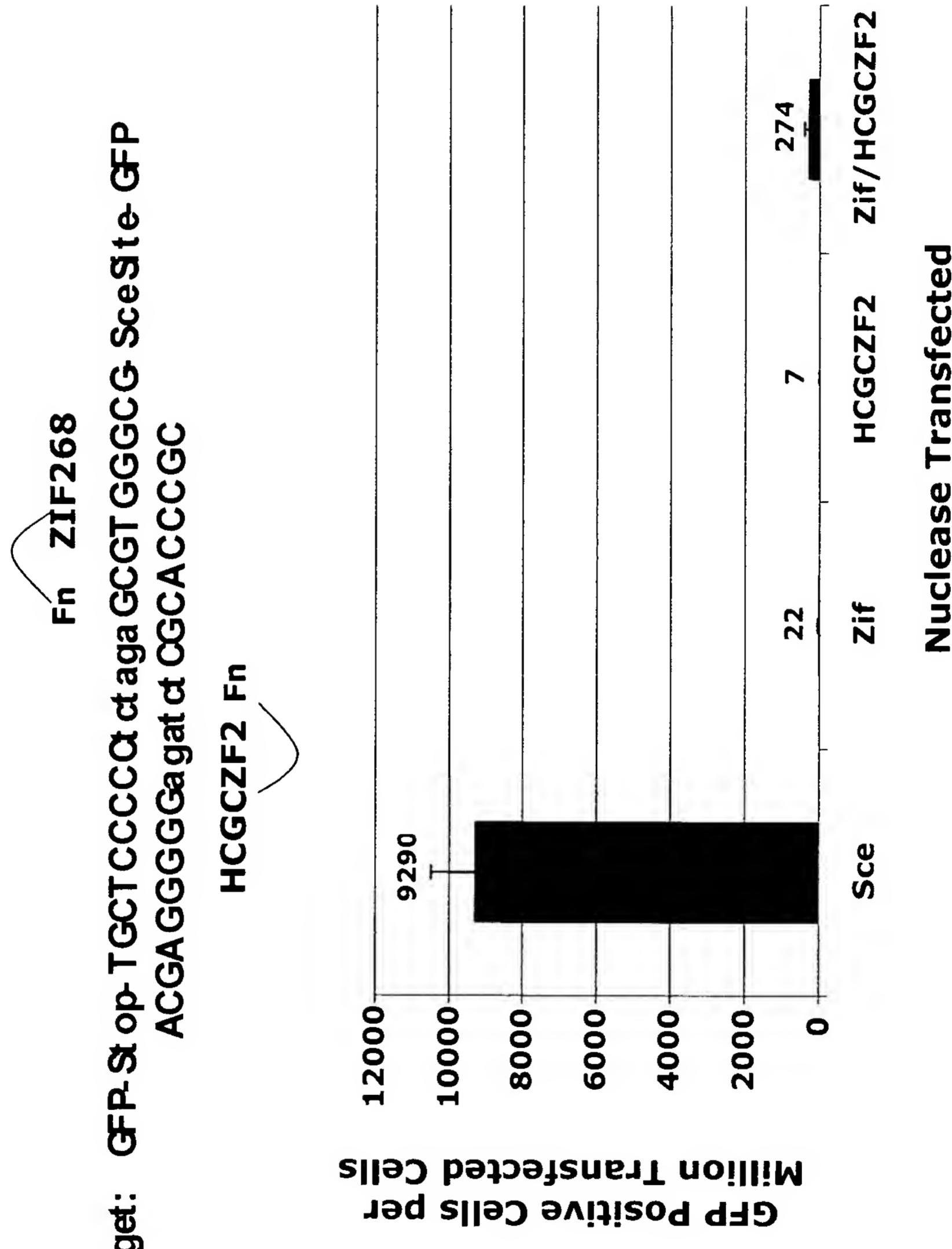


Fig. 12A



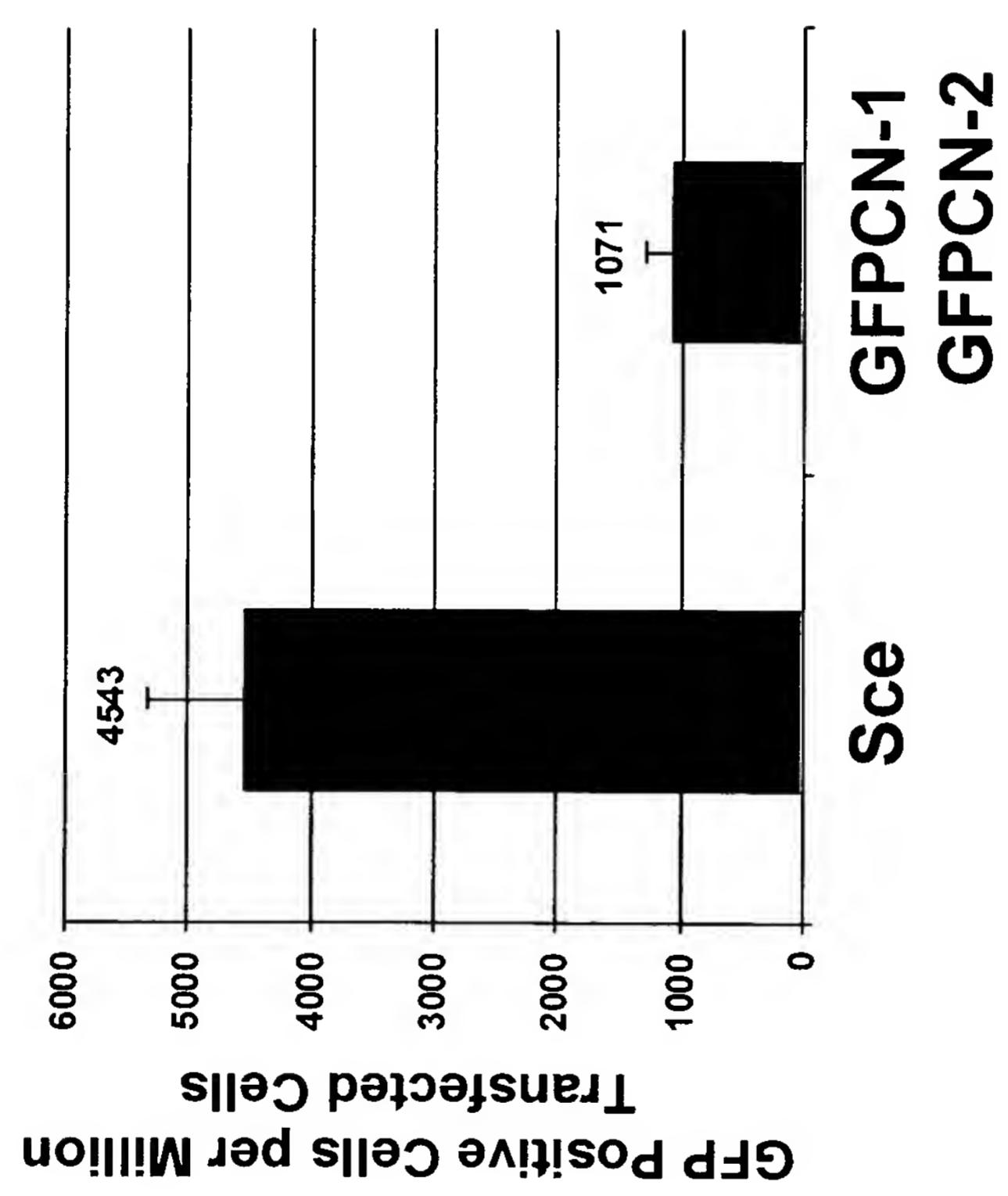


Fig. 12B

Fig. 13A

Fn  CD8ZF2  
bp 441 5 acc ggCgcCc a C cat cgc G cGca Gcc atg 3' bp 471  
tgg ccGcgGgt G gt agcgt CagCgt Cgg gac  
 CD8ZF1 

Fig. 13B

